

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: RICCARDI, Carlo
- (ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL DEATH PATHWAYS
- (iii) NUMBER OF SEQUENCES: 15
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
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(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 09/403,861
(B) FILING DATE: 11-FEB-2000
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP98/02490
(B) FILING DATE: 27-APR-1998
- vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: EP 97107033.9
(B) FILING DATE: 28-APR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: YUN, Allen C.
(B) REGISTRATION NUMBER: 37,971
(C) REFERENCE/DOCKET NUMBER: RICCARDI=1
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 206..616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTGGCTGCTG TGGAGTTTGT GACATACTAG GTGACACCCT TGGAGTCACT TCTCTTCAAC	60
TCCAGCTTAG AAGTGCCTGC CTGGCTCAGG GTCTGCACTG CAGCCTACTC CTTGCTTCAG	120
GGCCTGACTG CAACGCCAAA GCCTATCCTA TAGCGGCAGC GCCAGCAGCC ACTCAAACCA	180
GCCACAGCTC CCCGGCAACC GAACC ATG AAC ACC GAA ATG TAT CAG ACC CCC	232
Met Asn Thr Glu Met Tyr Gln Thr Pro	
1 5	
ATG GAG GTG GCG GTC TAT CAG CTG CAC AAT TTC TCC ACC TCC TTC TTT	280
Met Glu Val Ala Val Tyr Gln Leu His Asn Phe Ser Thr Ser Phe Phe	
10 15 20 25	
TCT TCT CTG CTT GGA GGG GAT GTG GTT TCC GTT AAA CTG GAT AAC AGT	328
Ser Ser Leu Leu Gly Gly Asp Val Val Ser Val Lys Leu Asp Asn Ser	
30 35 40	
GCC TCC GGA GCC AGT GTC GTC GTC GCC CTA GAC AAC AAG ATT GAG CAG GCC	376
Ala Ser Glu Ala Ser Val Val Ala Leu Asp Asn Lys Ile Glu Gln Ala	
45 50 55	
ATG GAC CTC GTG AAG AAC CAC CTG ATG TAC GCT GTG AGA GAG GAG GTG	424
Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val	
60 65 70	
GAG GTC CTA AAG GAG CAG ATT CGT GAG CTG CTT GAG AAG AAC TCC CAG	472
Glu Val Leu Lys Glu Gln Ile Arg Glu Leu Leu Glu Lys Asn Ser Gln	
75 80 85	
CTG GAG CGC GAG AAC ACC CTC CTG AAG ACG CTG GCA AGC CCC GAG CAA	520
Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln	
90 95 100 105	
CTG GAA AAG TTC CAG TCC CGG CTG AGC CCT GAA GAG CCA GCA CCT GAA	568
Leu Glu Lys Phe Gln Ser Arg Leu Ser Pro Glu Glu Pro Ala Pro Glu	
110 115 120	
GCC CCA GAA ACC CCG GAA ACC CCG GAA GCC CCT GGT GGT TCT GCG GTG	616
Ala Pro Glu Thr Pro Glu Thr Pro Glu Ala Pro Gly Gly Ser Ala Val	
125 130 135	
TAAGTGGCTC TGTCCTTAGG GTGGGCAGAG CCACATCTTG TTCTACCTAG TTCTTTCCAG	676
TTTGTTTTTG GTCCTCCAAG GGTCATCTCA TGTGGAGAAC TTTACACCTA ACATAGCTGG	736
TGCCAAGAGA TGTCCAAGG ACATGCCCCAT CTGGGTCCAC TCCAGTGACA GACCCCTGAC	796
AAAGAGCAGG TCTCTGGAGA CTAAGTTGCA TGGGGCCTAG TAACACCAAG CCAGTGAGCC	856
TGTCGTGTCA CCGGGCCCTG GGGGCTCCCA GGGCTGGGCA ACTTAGTTAC AGCTGACCAA	916
GGAGAAAGTA GTTTTGAGAT GTGATGCCAG TGTGCTCCAG AAAGTGTAAG GGGTCTGTTT	976
TTCATTTCCA TGGACATCTT CCACAGCTTC ACCTGACAAT GACTGTTCTT ATGAAGAAGC	1036
CACTTGTGTT CTAAGCAGAA GCAACCTCTC TCTTCTTCCT CTGTCTTTTC CAGGCAGGGG	1096
CAGAGATGGG AGAGATTGAG CCAAATGAGC CTTCTGTTGG TTAATACTGT ATAATGCATG	1156
GCTTTGTGCA CAGCCCAGTG TGGGGTTACA GCTTTGGGAT GACTGCTTAT AAAGTTCTGT	1216

TTGGTTAGTA TTGGCATCGT TTTTCTATAT AGCCATAATG CGTATATATA CCCATAGGGC	1276
TAGATCTATA TCTTAGGGTA GTGATGTATA CATATACACA TACACCTACA TGTGAAGGG	1336
CCTAACCAGC TTTGGGAGTA CTGACTGGTC TCTTATCTCT TAAAGCTAAG TTTTGGACTG	1396
TGCTAATTTA CCAAATTGAT CCAGTTTGTC CTTTAGATTA AATAAGACTC GATATGAGGG	1456
AGGGAGGGGA AGACCAGCCT CACAATGCGG CCACAGATGC CTTGCTGCTG CAGTCCTCCC	1516
TGATCTGTCC ACTGAAGACA TGAAGTCCTC TTTTGAATGC CAAACCCACC ATTCATTGGT	1576
GCTGACTACA TAGAATGGGG TTGAGAGAAG ATCAGTTTGG ACTTCACATT TTTGTTTTAA	1636
GTTTTAGGTT GTTTTTTTTT GGTTTTGTGT GTTTGTTTGT TTGTTTGTGT TGTTTTTTGT	1696
TTTTTCTTTT TTAAGTTCTT GTGGGGAAAC TTTGGGGTTA ATCAAAGGAT GTAGTCCTGT	1756
GGTAGACCAG AGGAGTAACT AGTTTTGATC CTTTGGGGTG TGGAAAATGT ACCCAGGAAG	1816
CTTGTGTAAG GAGGTTCTGT GACAGTGAAC ACTTTCCACT TTCTGACACC TCATCCTGCT	1876
GTACGACTCC AGGATTGGGA TTTGGATTTT TCAAATGTAG CTTGAAATTT CAATAAACTT	1936
TGCTCCTTTT TCTAAAATA AAAAAAAAAA AAAAAA	1972

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln	1	5	10	15
Leu His Asn Phe Ser Thr Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp	20	25	30	
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val	35	40	45	
Ala Leu Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His	50	55	60	
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile	65	70	75	80
Arg Glu Leu Leu Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu	85	90	95	
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Arg	100	105	110	
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ala Pro Glu Thr Pro Glu Thr	115	120	125	
Pro Glu Ala Pro Gly Gly Ser Ala Val	130	135		

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:1..20
 - (D) OTHER INFORMATION:/note= "PCR forward primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCATCTGGGT CCACTCCAGT

20

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION:1..20
 - (D) OTHER INFORMATION:/note= "PCR reverse primer"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AGGACAGTGG GAGTGGCACC

20

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1946 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION:241..642
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AATTCGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC

60

AACTCCAGCT GGAGCGCCTG CTTGGCTTTG GGTTCGTTCT GCAGCCTTCG CCCCCTCCT	120
AGCCTCAGGG CCGGACTCCA GCGCAGAGCC CAGCCCAGCG CAGCCTGCCA GCAGCCACCC	180
AGCCGCCCAG CCGCCCAGCC CCGCACGAAA CCCGGCCAGA GCTTCCTAGC AGCCCGAGCC	240
ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln	288
5 10 15	
CTG CAC AAT TTC TCC ATC TCC TTC TTC TCT TCT CTG CTT GGA GGG GAT Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp	336
20 25 30	
GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val	384
35 40 45	
GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His	432
50 55 60	
CTG ATG TAT GCT GTG AGA GAG GAG GTG GAG ATC CTG AAG GAG CAG ATC Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile	480
65 70 75 80	
CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu	528
85 90 95	
TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys	576
100 105 110	
CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala	624
115 120 125	
CCT GGT GGT TCT GCG GTG TAAGTGGCTC TGTCCTCAGG GTGGGCAGAG Pro Gly Gly Ser Ala Val	672
130	
CCACTAAACT TGTTTTACCT AGTTCTTTCC AGTTTGTTTT TGGCTCCCCA AGCATCATCT	732
CACGAGGAGA ACTTTACACC TAGCACAGCT GGTGCCAAGA GATGTCCTAA GGACATGGCC	792
ACCTGGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCAG GTCTCTGGAG GCTGAGTTGC	852
ATGGGGCCTA GTAACACCAA GCCAGTGAGC CTCTAATGCT ACTGCGCCCT GGGGGCTCCC	912
AGGGCCTGGG CAACTTAGCT GCAACTGGCA AAGGAGAAGG GTAGTTTGAG GTGTGACACC	972
AGTTTGCTCC AGAAAGTTTA AGGGGTCTGT TTCTCATCTC CATGGACATC TTCAACAGCT	1032
TCACCTGACA ACGACTGTTC CTATGAAGAA GCCACTTGTTG TTTTAAGCAG AGGCAACCTC	1092
TCTCTTCTCC TCTGTTTCGT GAAGGCAGGG GACACAGATG GGAGAGATTG AGCCAAGTCA	1152
GCCTTCTGTT GGTAAATATG GTATAATGCA TGGCTTTGTG CACAGCCCAG TGTGGGATTA	1212
CAGCTTTGGG ATGACCGCTT ACAAAGTTCT GTTTGGTTAG TATTGGCATA GTTTTTCTAT	1272
ATAGCCATAA ATGCGTATAT ATACCCATAG GGCTAGATCT GTATCTTAGT GTAGCGATGT	1332

ATACATATAC ACATCCACCT ACATGTTGAA GGGCCTAACC AGCCTTGGGA GTATTGACTG	1392
GTCCCTTACC TCTTATGGCT AAGTCTTTGA CTGTGTTTCAT TTACCAAGTT GACCCAGTTT	1452
GTCTTTTtagg TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCCTCTGAAT	1512
GCGGCCACGG ATGCCTTGCT GCTGCAACCC TTTCCCCAGC TGTCCACTGA AACGTGAAGT	1572
CCTGTTTTGA ATGCCAAACC CACCATTAC TGGTGCTGAC TACATAGAAT GGGTTGAGAG	1632
AAGATCAGTT TGGGCTTCAC AGTGTCATTT GAAAAAGCGT TTTTGTTTTG TTTTGAATTA	1692
TTGTGGAAAA CTTTCAAGTG AACAGAAGGA TGGTGTCTTA CTGTGGATGA GGGATGAACA	1752
AGGGGATGGC TTTGATCCAA TGGAGCCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG	1812
GGTTTTGTGA GAGTGAACAC TTTCCACTTT TTGACACCTT ATCCTGATGT ATGGTTCCAG	1872
GATTTGGATT TTGATTTTCC AAATGTAGCT TGAAATTTCA ATAAACTTTG CTCTGTTTTT	1932
CTAAAAAATA AAAA	1946

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Asn	Thr	Glu	Met	Tyr	Gln	Thr	Pro	Met	Glu	Val	Ala	Val	Tyr	Gln
1				5					10					15	
Leu	His	Asn	Phe	Ser	Ile	Ser	Phe	Phe	Ser	Ser	Leu	Leu	Gly	Gly	Asp
			20					25					30		
Val	Val	Ser	Val	Lys	Leu	Asp	Asn	Ser	Ala	Ser	Gly	Ala	Ser	Val	Val
		35					40					45			
Ala	Ile	Asp	Asn	Lys	Ile	Glu	Gln	Ala	Met	Asp	Leu	Val	Lys	Asn	His
	50					55					60				
Leu	Met	Tyr	Ala	Val	Arg	Glu	Glu	Val	Glu	Ile	Leu	Lys	Glu	Gln	Ile
65					70				75					80	
Arg	Glu	Leu	Val	Glu	Lys	Asn	Ser	Gln	Leu	Glu	Arg	Glu	Asn	Thr	Leu
			85						90					95	
Leu	Lys	Thr	Leu	Ala	Ser	Pro	Glu	Gln	Leu	Glu	Lys	Phe	Gln	Ser	Cys
		100						105					110		
Leu	Ser	Pro	Glu	Glu	Pro	Ala	Pro	Glu	Ser	Pro	Gln	Val	Pro	Glu	Ala
		115					120					125			
Pro	Gly	Gly	Ser	Ala	Val										
		130													

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Leu Lys Glu Gln Ile Lys Glu Leu Ile Glu Lys Asn Ser Gln Leu Glu
1 5 10 15
Gln Glu Asn Asp Leu Leu Lys Thr Leu Ala
20 25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu
1 5 10 15
Asn Glu Val Ala Arg Leu Lys Lys Leu Val
20 25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile
1 5 10 15
Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln Asn Lys Thr Leu Ile
1 5 10 15

Glu Glu Leu Lys Ala Leu Lys Asp Leu Tyr
20 25

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn Ser Glu Leu Ala
1 5 10 15
Ser Thr Ala Asn Met Leu Arg Glu Gln Val
20 25

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val
1 5 10 15
Glu Ile Leu Lys Glu Gln Ile Arg Glu Leu Val Glu Lys Asn Ser Gln
20 25 30
Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln
35 40 45
Leu Glu Lys Phe Gln Ser Cys Leu Ser Pro Glu Glu Pro Ala Pro Glu
50 55 60
Ser Pro Gln Val Pro Glu Ala Pro Gly Gly Ser Ala Val
65 70 75

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 143 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Lys Ser Gln Trp Cys Arg Pro Val Ala Met Asp Leu Gly Val Tyr Gln
1 5 10 15
Leu Arg His Phe Ser Ile Ser Phe Leu Ser Ser Leu Leu Gly Thr Glu
20 25 30

Asn	Ala	Ser	Val	Arg	Leu	Asp	Asn	Ser	Ser	Ser	Gly	Ala	Ser	Val	Val
		35					40					45			
Ala	Ile	Asp	Asn	Lys	Ile	Glu	Gln	Ala	Met	Asp	Leu	Val	Lys	Ser	His
	50				55						60				
Leu	Met	Tyr	Ala	Val	Arg	Glu	Glu	Val	Glu	Val	Leu	Lys	Glu	Gln	Ile
	65				70					75					80
Lys	Glu	Leu	Ile	Glu	Lys	Asn	Ser	Gln	Leu	Glu	Gln	Glu	Asn	Asn	Leu
			85						90					95	
Leu	Lys	Thr	Leu	Ala	Ser	Pro	Glu	Gln	Leu	Ala	Gln	Phe	Gln	Ala	Gln
			100					105						110	
Leu	Gln	Thr	Gly	Ser	Pro	Pro	Ala	Thr	Thr	Gln	Pro	Gln	Gly	Thr	Thr
		115					120					125			
Gln	Pro	Pro	Ala	Gln	Pro	Ala	Ser	Gln	Gly	Ser	Gly	Pro	Thr	Ala	
	130					135					140				

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION:/note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with a-(4-methyl-coumaryl-7-amide)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Asp Glu Val Asp

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION:/note= "the N-terminus is modified by an acetyl group; the C-terminus is modified with CH₂OC(O)-[2,6-(CF₃)₂]Ph"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Tyr Val Ala Asp